

(5') 1 SDLEQERRAKEKLQEQQ  
18 SDLEQDRLAKEKLQEQQ  
35 SDLEQERLAKEKLQEQQ  
52 SDLEQERRAKEKLQEQQ  
69 SDLEQERRAKEKLQEQQ  
86 SDLEQDRLAKEKLQEQQ  
103 SDLEQERRAKEKLQEQQ  
120 SDLEQERKAKEKLQEQQ  
137 SDLEQERLAKEKLQEQQ  
154 SDLEQERRAKEKLQEQQ  
171 SDLEQERRAKEKLQEQQ  
188 SDLEQERRAKEKLQEQQ  
205 RDLEQ  
  
210 RKADTKKNLERKKEHGDILAEDLYGRLEIP  
240 AIELPSENERGYYPHQSSLPQDNRGNSRD  
270 SKEISIIIEKTNRESITTNVEGRRDIHKGHL  
300 EEKKDGSIKPEQKEDKS 316 (3')

FIGURE 1

09837344.041901  
106140-44E2E860

106140-44E/CE60

(5') 1 AAAGCGATCTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 52 AAAGCGATTTAGAACACAGATAGACTTGCTAAAGAAAAAGTTACAGAGCAGC  
 103 AAAGCGATTTAGAACACAGAGAGACTTGCTAAAGAAAAAGTTGCAAGAACAA  
 154 AAAGCGATCTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 205 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 256 AAAGCGATTTAGAACACAGATAGACTTGCTAAAGAAAAAGTTACAGAGCAGC  
 307 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 358 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 409 AAAGCGATTTAGAACACAGAGAGACTTGCTAAAGAAAAAGTTGCAAGAACAA  
 460 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 511 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 562 AAAGCGATTTAGAACACAGAGAGACGTGCTAAAGAAAAAGTTGCAAGAACAA  
 613 AAAGCGATTTAGAACAA  
 630 AGGAAGGCTGATACGAAAAAAAATTTAGAAAAAAAAGGAACATGGAGAT  
 681 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT  
 732 CCATCAGAAAATGAACGTGGATATTATATACCAATCAATCTCTTTACCT  
 783 CAGGCAACACAGAGGGAATAGTAGAGATTCAGGAAATATCTATATAGAA  
 834 AAAACAAATAGAGAACTATTACAACAATGTTGAAGGACGAGGATATA  
 885 CATAAGGACATCTTGAAGAAAAAGAAAGATGGTTCAATAAAACCAGAACAA  
 936 AAAGAAGATAAATCT 950 (3')

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDIDFNSLVKSVQQEQQ  
HNVEEKVEESVEENDEESVEENVEENVEENDDGSSVASSVEESI  
ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE  
ESVAPSVEESVAEMLKER

## FIGURE 3

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT  
 GTT AAT GGA GAA GTA AAA GAA AAT ATT TTG GAG GAA AGT CAA GTT AAT  
 GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA  
 CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG  
 AAG AAA GTG TAG AAG AAA ATG TAG AAG AAA ATG TAG AAG AAA ATG  
 ACG ACG GAA GTG TAG CCT CAA GTG TTG AAG AAA GTA TAG CTT CAA GTG  
 TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG AAA ATG TAG CTC CAA CTG  
 TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG AAA TTG TAG CTC CAA GTG  
 TTG TAG AAA AGT GTG CTC CAA GTG TTG AAG AAA GTG TAG CTC CAA GTG  
 TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

106440" 44EZE860

NSRDSKEISIIIEKTNRESITTNVEGRDDIHK

LSA-TER

DELFNELLNSVDVNGEVKENILEESQ  
LEESQVNDIDIFNSLVKSVDQEQOHNV  
VEKCAPSVEESVAPSVEESVAEMLKER

729S-NRI  
729S-NRII  
729S-Rep

FIGURE 5

**NUCLEOTIDE SEQUENCE OF THE LSA GENE**  
**5' END**

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG  
84 ATATTTTCATATAAATGGAAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA  
135 TAAATCTAACTTGAGAAGTGTTCTTCAAATTTCTAGGAATCGAATAAATGA  
186 GGAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAAT  
237 AAAAAATATGAAAAATAAATTTTTTCGATAAGGATAAAGAGTTAACGATGT  
288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAGTCTTTTAAGAAATCT  
339 TGGTGTTTCAGAGAATATATTCCTTAAAGAAAAATAATTAATAAGGAAGGG  
390 AAATTAATTGAACACATAATAATGATGATGACGATAAAAAAATATATTA  
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAAGTTACAGGGGCAACAAAGCGATTAGAACAAGAGAGACGT  
543 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT  
594 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
645 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT  
696 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
747 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
798 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT  
849 GCTAAAGAAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT  
900 GCTAAAGAAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT  
951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

**FIGURE 6**

LSA.5'/ATG - -> 1-phase Translation	DNA sequence	956 b.p. ATGAACATATT ... AAGCGATTTAGA	linear
1 / 1	ATG AAA CAT ATT TTG TAC ATA TCA TTT TAC TTT ATC CTT GTT AAT TTA TTG ATA TTT CAT	met lys his ile leu tyr ile ser phe tyr phe ile leu val asn leu leu ile phe his	61 / 21
1 / 1	ATA AAT GGA AAG ATA ATA AAG AAT TCT GAA AAA GAT GAA ATC ATA AAA TCT AAC TTG AGA	ile asn gly lys ile ile lys asn ser glu lys asp glu ile ile lys ser asn leu arg	121 / 41
1 / 1	AGT GGT TCT TCA AAT TCT AGG AAT CGA ATA AAT GAG GAA AAT CAC GAG AAG AAA CAC GTT	arg gly ser ser asn ser arg asn arg ile asn glu glu asn his glu lys lys his val	181 / 61
1 / 1	TTA TCT CAT AAT TCA TAT GAG AAA ACT AAA AAT AAT GAA AAT AAT AAA TTT TTC GAT AAG	leu ser his asn ser tyr glu lys thr lys asn asn glu asn asn lys phe phe asp lys	241 / 81
1 / 1	GAG TTA ACG ATG TCT AAT GTA AAA AAT GTG TCA CAA ACA AAT TTC AAA AGT CTT	asp lys glu leu thr met ser asn val lys asn val ser gln thr asn phe lys ser leu	301 / 101
1 / 1	TTA AGA AAT CTT GGT GTT TCA GAG AAT ATA TTC CTT AAA GAA AAT AAA TTA AAT AAG GAA	leu arg asn leu gly val ser glu asn ile phe leu lys glu asn lys leu asn lys glu	361 / 121

FIGURE 7A

FIGURE 7B



781	/	261	811	/	271	
CAA	GAA	CAA	CAA	GAG	AGA	CTT GCT AAA GAA AAG TTA CAA GAG CAG
gln	glu	gln	gln	glu	arg	leu ala lys glu lys leu gln glu gln
841	/	281	871	/	291	
CAA	AGC	GAT	TTA	GAA	GAT	AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT
gln	ser	asp	leu	glu	asp	arg leu ala lys glu lys leu gln glu gln ser asp
901	/	301	931	/	311	
TTA	GAA	CAA	GAG	AGA	CGT	GCT AAA GAA AGG TTG CAA GAA CAA AGC GAT TTA
leu	glu	gln	glu	arg	ala	lys glu arg leu gln glu gln ser asp leu

FIGURE 7C

**NUCLEOTIDE SEQUENCE OF THE LSA GENE**  
**3' END**

(CODING 3' END, REPETITIVE)

1 CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT  
37 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT  
88 GCTAAAGAAAAGTTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT  
139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT  
190 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAGACGT  
241 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT  
292 GCTAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGAGACGT  
343 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAGACGT  
394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT  
445 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAGACGT  
496 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAGACGT  
547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGAGACGT  
598 GCTAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAGGAACATGGAGAT  
691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT  
742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT  
793 CAGGACAACAGAGGGAATAGTAGAGATTTCCAAGGAAATATCTATAATAGAA  
844 AAAACAATAGAGAATCTATTACAACAATGTTGAAGGACGAAGGGATATA  
895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCATATAAACCCAGAACAA  
946 AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT  
997 ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT  
1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT  
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA  
1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT  
1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG  
1252 AAAAAATAAAAAAAGGAAAGAAATATGAAAAACAAAGGATAATAATTTTA  
1303 AACCAATGATAAAAGTTTGTATGATGAGCATATTAATAATATAAAAAATG  
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTTGTTTCATA  
1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG  
1456 ATATACTAAATATTTTATGAACTATAA (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

**FIGURE 8**

0837.244 041901  
106140 +42860

LSA.3'.ALL -> 1-phase Translation

DNA sequence 1496 b.p. CAAGAACAAACA ... GGTATATATTT linear

1 / 1	31 / 11	
CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA		
gln glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln glu gln		
61 / 21	91 / 31	
CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT		
gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp		
121 / 41	151 / 51	
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT CTA GAA CAA		
leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu glu gln		
181 / 61	211 / 71	
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG AGA CGT		
glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln gln arg		
241 / 81	271 / 91	
GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA		
ala lys glu lys leu gln glu gln gln ser asp leu glu gln asp arg leu ala lys glu		
301 / 101	331 / 111	
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAG TTG CAA		
lys leu gln glu gln gln ser asp leu glu gln glu arg ala lys lys leu gln		

FIGURE 9A

361 / 121 391 / 131  
 GAA CAA CAA AGC GAT TTA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA  
 glu gln glu ser asp leu glu gln glu arg arg ala lys glu lys leu gln glu gln gln  
 421 / 141 451 / 151  
 AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA  
 ser asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu  
 481 / 161 511 / 171  
 GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG  
 glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu  
 541 / 181 571 / 191  
 AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT  
 arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu arg ala  
 601 / 201 631 / 211  
 AAA GAA AAG TTG CAA GAG CAG CAA AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA  
 lys glu lys leu gln glu gln gln arg asp leu glu gln arg lys ala asp thr lys lys  
 661 / 221 691 / 231  
 AAT TTA GAA AGA AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA  
 asn leu glu arg lys lys glu his gly asp ile leu ala glu asp leu tyr gly arg leu  
 721 / 241 751 / 251  
 GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA  
 glu ile pro ala ile glu leu pro ser glu asn glu arg gly tyr tyr ile pro his gln  
 781 / 261 811 / 271  
 TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA  
 ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile

FIGURE 9B

106140" 44E2E860

841 / 281	871 / 291	
GAA AAA ACA AAT AGA GAA TCT ATT ACA ACA AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA		
glu lys thr asn arg glu ser ile thr thr asn val glu gly arg asp ile his lys		
901 / 301	931 / 311	
GGA CAT CTT GAA AAG AAA GAT GGT TCA ATA AAA CCA GAA CAA AAA GAA GAT AAA TCT		
gly his leu glu glu lys lys asp gly ser ile lys pro glu gln lys glu asp lys ser		
961 / 321	991 / 331	
GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA		
ala asp ile gln asn his thr leu glu thr val asn ile ser asp val asn asp phe gln		
1021 / 341	1051 / 351	
ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA		
ile ser lys tyr glu asp glu ile ser ala glu tyr asp asp ser leu ile asp glu glu		
1081 / 361	1111 / 371	
GAA GAT GAT GAA GAC TTA GAC GAA TTT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT		
glu asp asp glu asp leu asp glu phe lys pro ile val gln tyr asp asn phe gln asp		
1141 / 381	1171 / 391	
GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA		
glu glu asn ile gly ile tyr lys glu leu glu asp leu ile glu lys asn glu asn leu		
1201 / 401	1231 / 411	
GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA GAA AAA ATA AAA		
asp asp leu asp asp glu gly ile glu lys ser ser glu glu leu ser glu glu lys ile lys		

FIGURE 9C

106140- the 25860

1261 / 421	1291 / 431	
AAA GGA AAG AAA TAT GAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG		
lys gly lys lys tyr glu lys thr lys asp asp asn phe lys pro asn asp lys ser leu		
1321 / 441	1351 / 451	
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA		
tyr asp glu his ile lys lys tyr lys asp lys gln val asn lys glu lys glu lys		
1381 / 461	1411 / 471	
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT		
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp		
1441 / 481	1471 / 491	
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT		
glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr		

FIGURE 9D

DNA sequence 1482 b.p. CAAGAACAACAA ... ATGAAACTATAA linear

[illegible]

FIGURE 10A

361 / 121 391 / 131  
 GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA  
 glu gln gln ser asp leu 451 / 151  
 421 / 141  
 AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA  
 ser asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln ser asp leu  
 481 / 161 511 / 171  
 GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG  
 glu gln glu arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln glu  
 541 / 181 571 / 191  
 AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT  
 arg arg ala lys glu lys leu gln glu gln gln gln ser asp leu glu gln glu arg arg ala  
 601 / 201 631 / 211  
 AAA GAA AAG TTG CAA GAG CAG CAA AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA  
 lys glu lys leu gln glu gln gln arg asp leu glu gln arg lys ala asp thr lys lys  
 661 / 221 691 / 231  
 AAT TTA GAA AGA AAA AAG GAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA  
 asn leu glu arg lys lys glu his gln gln gln gln gln gln gln gln gln gln gln gln gln  
 721 / 241 751 / 251  
 GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA  
 glu ile pro ala ile glu leu pro ser glu asn glu arg gly tyr tyr ile pro his gln  
 781 / 261 811 / 271  
 TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA  
 ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile

FIGURE 10B



106140"44E2950

841 / 281	GAA AAA ACA AAT AGA GAA	871 / 291	TCT ATT ACA ACA AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA
901 / 301	glu lys thr asn arg glu ser ile thr thr asn val glu gly arg asp ile his lys	931 / 311	
GGA CAT CTT GAA GAA AAG AAA GAT GGT TCA ATA AAA CCA GAA CAA AAA GAA GAT AAA TCT			
961 / 321	gly his leu glu glu lys lys asp gly ser ile lys pro glu gln lys glu asp lys ser	991 / 331	
GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA			
1021 / 341	ala asp ile gln asn his thr leu glu thr val asn ile ser asp val asn asp phe gln	1051 / 351	
ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA			
1081 / 361	ile ser lys tyr glu asp glu ile ser ala glu tyr asp asp ser leu ile asp glu glu	1111 / 371	
GAA GAT GAT GAA GAC TTA GAC GAA TTT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT			
1141 / 381	glu asp asp glu asp leu asp glu phe lys pro ile val gln tyr asp asn phe gln asp	1171 / 391	
GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA			
1201 / 401	glu glu asn ile gly ile tyr lys glu leu glu asp leu ile glu lys asn glu asn leu	1231 / 411	
GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA GAA ATA AAA			
1261 / 421	asp asp leu asp glu gly ile glu lys ser ser glu glu leu ser glu glu lys ile lys	1291 / 431	
AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG			
lys gly lys lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu			

FIGURE 10C

1321 / 441 1351 / 451  
 TAT GAT GAG CAT ATT AAA TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA  
 tyr asp glu his ile lys lys tyr lys asp lys gln val asn lys glu lys glu lys  
 1381 / 461 1411 / 471  
 TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT  
 phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp  
 1441 / 481 1471 / 491  
 GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT  
 glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr

FIGURE 10D